

SEQUENCE LISTING

<110> Alessi, Dario
Balendran, Anudharan
Deak, Maria
Currie, Richard
Downes, Peter
Casamayor, Antonio

<120> Enzyme

<130> 002.00170

<140> US 09/937,009

<141> 2000-03-17

<150> PCT/GB00/01004

<151> 2000-03-17

<150> GB 9906245.7

<151> 1999-03-19

<160> 34

<170> PatentIn Ver. 2.1

<210> 1

<211> 24

<212> PRT

<213> Homo sapiens

<220>

<223> region B of PRK2

<400> 1

Arg Glu Pro Arg Ile Leu Ser Glu Glu Glu Gln Glu Met Phe Arg Asp

1 5 10 15

Phe Asp Tyr Ile Ala Asp Trp Cys

20

<210> 2

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
peptide sequence that interacts with human PRK2
region B

<400> 2

Arg Glu Pro Arg Ile Leu Ser Glu Glu Glu Gln Glu Met Ala Arg Asp
1 5 10 15

Phe Asp Tyr Ile Ala Asp Trp Cys
20

<210> 3

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
peptide sequence that interacts with human PRK2
region B

<400> 3

Arg Glu Pro Arg Ile Leu Ser Glu Glu Glu Gln Glu Met Phe Gly Asp
1 5 10 15

Phe Asp Tyr Ile Ala Asp Trp Cys
20

<210> 4

<211> 53

<212> PRT

<213> Homo sapiens

<220>

<223> region A of PRK2

<400> 4

Glu Asp Val Lys Lys His Pro Phe Phe Arg Leu Ile Asp Trp Ser Ala
1 5 10 15

Leu Met Asp Lys Lys Val Lys Pro Pro Phe Ile Pro Thr Ile Arg Gly
20 25 30

Arg Glu Asp Val Ser Asn Phe Asp Asp Glu Phe Thr Ser Glu Ala Pro
35 40 45

Ile Leu Thr Pro Pro

50

<210> 5

<211> 23

<212> PRT

<213> Homo sapiens

<220>

<223> region of PKC zeta

<400> 5

Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser Glu Phe Glu Gly Phe

1

5

10

15

Glu Tyr Ile Asn Pro Leu Leu

20

<210> 6

<211> 6

<212> PRT

<213> Homo sapiens

<220>

<223> portion of region B of PRK2

<400> 6

Phe Arg Asp Phe Asp Tyr

1

5

<210> 7

<211> 23

<212> PRT

<213> Homo sapiens

<220>

<223> region of PKC zeta

<400> 7

Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser Glu Phe Glu Gly Phe

1

5

10

15

Glu Tyr Ile Asn Pro Leu Leu

20

<210> 8
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<223> region of PKB alpha

<400> 8
Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser
1 5 10

<210> 9
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> region of PRK1

<400> 9
Thr Phe Cys Gly Thr Pro Glu Phe Leu
1 5

<210> 10
<211> 6
<212> PRT
<213> Homo sapiens

<220>
<223> region of PKC zeta

<400> 10
Phe Glu Gly Phe Glu Tyr
1 5

<210> 11
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<223> region of PDK1

<400> 11

Arg Gln Arg Tyr Gln Ser His Pro Asp Ala Ala Val Gln
1 5 10

<210> 12

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:pcr primer

<400> 12

cgggatccga ggatgtaaaa aagcaccc

28

<210> 13

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:human PKB alpha
substrate peptide

<400> 13

Arg Pro Arg Thr Ala Phe
1 5

<210> 14

<211> 77

<212> PRT

<213> Homo sapiens

<220>

<223> region of PRK2

<400> 14

Glu Asp Val Lys Lys His Pro Phe Phe Arg Leu Ile Asp Trp Ser Ala
1 5 10 15

Leu Met Asp Lys Lys Val Lys Pro Pro Phe Ile Pro Thr Ile Arg Gly
20 25 30

Arg Glu Asp Val Ser Asn Phe Asp Asp Glu Phe Thr Ser Glu Ala Pro
35 40 45

Ile Leu Thr Pro Pro Arg Glu Pro Arg Ile Leu Ser Glu Glu Glu Gln
50 55 60

Glu Met Phe Arg Asp Phe Asp Tyr Ile Ala Asp Trp Cys
65 70 75

<210> 15
<211> 77
<212> PRT
<213> Homo sapiens

<220>
<223> region of PRK1

<400> 15
Glu Asp Val Lys Lys Gln Pro Phe Phe Arg Thr Leu Gly Trp Glu Ala
1 5 10 15

Leu Leu Ala Arg Arg Leu Pro Pro Pro Phe Val Pro Thr Leu Ser Gly
20 25 30

Arg Thr Asp Val Ser Asn Phe Asp Glu Glu Phe Thr Gly Glu Ala Pro
35 40 45

Thr Leu Ser Pro Pro Arg Asp Ala Arg Pro Leu Thr Ala Ala Glu Gln
50 55 60

Ala Ala Phe Leu Asp Phe Asp Phe Val Ala Gly Gly Cys
65 70 75

<210> 16
<211> 80
<212> PRT
<213> Homo sapiens

<220>
<223> region of PKB alpha

<400> 16
Lys Glu Ile Met Gln His Arg Phe Phe Ala Gly Ile Val Trp Gln His
1 5 10 15

Val Tyr Glu Lys Lys Leu Ser Pro Pro Phe Lys Pro Gln Val Thr Ser
20 25 30

Glu Thr Asp Thr Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Met Ile
35 40 45

Thr Ile Thr Pro Pro Asp Gln Asp Asp Ser Met Glu Cys Val Asp Ser
50 55 60

Glu Arg Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Thr Ala
65 70 75 80

<210> 17
<211> 75
<212> PRT
<213> Homo sapiens

<220>
<223> region of P70S6k

<400> 17
Gly Glu Val Gln Ala His Pro Phe Phe Arg His Ile Asn Trp Glu Glu
1 5 10 15

Leu Leu Ala Arg Lys Val Glu Pro Pro Phe Lys Pro Leu Leu Gln Ser
20 25 30

Glu Glu Asp Val Ser Gln Phe Asp Ser Lys Phe Thr Arg Gln Thr Pro
35 40 45

Val Asp Ser Pro Asp Asp Ser Thr Leu Ser Glu Ser Ala Asn Gln Val
50 55 60

Phe Leu Gly Phe Thr Tyr Val Ala Pro Ser Val
65 70 75

<210> 18
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<223> region of SGK

<400> 18
Met Glu Ile Lys Ser His Val Phe Phe Ser Leu Ile Asn Trp Asp Asp

<220>

<223> region of PKC alpha

<400> 20

Arg Asp Val Arg Glu His Ala Phe Phe Arg Arg Ile Asp Trp Glu Lys

1

5

10

15

Leu Glu Asn Arg Glu Ile Gln Pro Pro Phe Lys Pro Lys Val Cys Gly

20

25

30

Lys Gly Ala Glu Asn Phe Asp Lys Phe Phe Thr Arg Gly Gln Pro Val .

35

40

45

Leu Thr Pro Pro Asp Gln Leu Val Ile Ala Asn Ile Asp Gln Ser Asp

50

55

60

Phe Glu Gly Phe Ser Tyr Val Asn Pro Gln Phe

65

70

75

<210> 21

<211> 62

<212> PRT

<213> Homo sapiens

<220>

<223> region of PKA beta

<400> 21

Ser Asp Ile Lys Thr His Lys Trp Phe Ala Thr Thr Asp Trp Ile Ala

1

5

10

15

Ile Tyr Gln Arg Lys Val Glu Ala Pro Phe Ile Pro Lys Phe Gly Arg

20

25

30

Ser Gly Asp Thr Ser Asn Phe Asp Asp Tyr Glu Glu Glu Asp Ile Arg

35

40

45

Val Ser Ile Thr Glu Cys Ala Lys Glu Lys Phe Gly Glu Phe

50

55

60

<210> 22

<211> 6

<212> PRT

<213> Homo sapiens

<220>

<223> PKB consensus sequence

<220>

<223> residues 2 and 3 are variable amino acids

<400> 22

Phe Xaa Xaa Phe Ser Phe

1 5

<210> 23

<211> 8

<212> PRT

<213> Homo sapiens

<220>

<223> PKB consensus sequence

<220>

<223> residue 6 is a variable amino acid

<400> 23

Thr Phe Cys Gly Thr Xaa Glu Leu

1 5

<210> 24

<211> 6

<212> PRT

<213> Homo sapiens

<220>

<223> PKB consensus sequence

<220>

<223> residues 2 and 3 are variable amino acids

<220>

<223> residue 5 is serine or threonine

<220>

<223> residue 6 is phenylalanine or tyrosine

<400> 24

Phe Xaa Xaa Phe Xaa Xaa

1 5

<210> 25
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 sequence that interacts with PKB

<220>
 <223> residues 2 and 3 are variable amino acids

<220>
 <223> residues 1, 4 and 6 are phenylalanine or tyrosine

<220>
 <223> residue 5 is a negatively charged amino acid

<400> 25
 Xaa Xaa Xaa Xaa Xaa Xaa
 1 5

<210> 26
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 sequence that interacts with PKB

<220>
 <223> residues 2 and 3 are variable amino acids

<220>
 <223> residues 1, 4 and 6 are phenylalanine or tyrosine

<220>
 <223> residue 5 is aspartic acid or glutamic acid

<400> 26
 Xaa Xaa Xaa Xaa Xaa Xaa
 1 5

<210> 27
 <211> 6

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 sequence that interacts with PKB

<220>
 <223> residues 2 and 3 are variable amino acids

<220>
 <223> residues 1, 4 and 6 are phenylalanine or tyrosine

<220>
 <223> residue 5 is phospho serine or phospho threonine

<400> 27
 Xaa Xaa Xaa Xaa Xaa Xaa
 1 5

<210> 28
 <211> 8
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PKB consensus sequence

<220>
 <223> residue 1 is threonine or serine

<220>
 <223> residue 6 is a variable amino acid

<400> 28
 Xaa Phe Cys Gly Thr Xaa Glu Leu
 1 5

<210> 29
 <211> 6
 <212> PRT
 <213> Homo sapiens

<220>
 <223> C terminal region of PKC zeta

Leu	Gln	His	Ala	Gln	Pro	Pro	Gln	Pro	Arg	Lys	Lys	Arg	Pro	Glu	
65					70				75					80	
Asp	Phe	Lys	Phe	Gly	Lys	Ile	Leu	Gly	Glu	Gly	Ser	Phe	Ser	Thr	Val
				85					90					95	
Val	Leu	Ala	Arg	Glu	Leu	Ala	Thr	Ser	Arg	Glu	Tyr	Ala	Ile	Lys	Ile
			100					105					110		
Leu	Glu	Lys	Arg	His	Ile	Ile	Lys	Glu	Asn	Lys	Val	Pro	Tyr	Val	Thr
		115					120					125			
Arg	Glu	Arg	Asp	Val	Met	Ser	Arg	Leu	Asp	His	Pro	Phe	Phe	Val	Lys
	130					135					140				
Leu	Tyr	Phe	Thr	Phe	Gln	Asp	Asp	Glu	Lys	Leu	Tyr	Phe	Gly	Leu	Ser
145					150					155					160
Tyr	Ala	Lys	Asn	Gly	Glu	Leu	Leu	Lys	Tyr	Ile	Arg	Lys	Ile	Gly	Ser
				165					170					175	
Phe	Asp	Glu	Thr	Cys	Thr	Arg	Phe	Tyr	Thr	Ala	Glu	Ile	Val	Ser	Ala
			180					185					190		
Leu	Glu	Tyr	Leu	His	Gly	Lys	Gly	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro
		195					200					205			
Glu	Asn	Ile	Leu	Leu	Asn	Glu	Asp	Met	His	Ile	Gln	Ile	Thr	Asp	Phe
	210					215					220				
Gly	Thr	Ala	Lys	Val	Leu	Ser	Pro	Glu	Ser	Lys	Gln	Ala	Arg	Ala	Asn
225					230					235					240
Ser	Phe	Val	Gly	Thr	Ala	Gln	Tyr	Val	Ser	Pro	Glu	Leu	Leu	Thr	Glu
				245					250					255	
Lys	Ser	Ala	Cys	Lys	Ser	Ser	Asp	Leu	Trp	Ala	Leu	Gly	Cys	Ile	Ile
			260					265					270		
Tyr	Gln	Leu	Val	Ala	Gly	Leu	Pro	Pro	Phe	Arg	Ala	Gly	Asn	Glu	Tyr
		275					280					285			
Leu	Ile	Phe	Gln	Lys	Ile	Ile	Lys	Leu	Glu	Tyr	Asp	Phe	Pro	Glu	Lys
	290						295				300				
Phe	Phe	Pro	Lys	Ala	Arg	Asp	Leu	Val	Glu	Lys	Leu	Leu	Val	Leu	Asp
305					310					315					320

Ala	Thr	Lys	Arg	Leu	Gly	Cys	Glu	Glu	Met	Glu	Gly	Tyr	Gly	Pro	Leu	
				325					330						335	
Lys	Ala	His	Pro	Phe	Phe	Glu	Ser	Val	Thr	Trp	Glu	Asn	Leu	His	Gln	
			340					345					350			
Gln	Thr	Pro	Pro	Lys	Leu	Thr	Ala	Tyr	Leu	Pro	Ala	Met	Ser	Glu	Asp	
		355					360					365				
Asp	Glu	Asp	Cys	Tyr	Gly	Asn	Tyr	Asp	Asn	Leu	Leu	Ser	Gln	Phe	Gly	
	370					375					380					
Cys	Met	Gln	Val	Ser	Ser	Ser	Ser	Ser	Ser	His	Ser	Leu	Ser	Ala	Ser	
385				390						395					400	
Asp	Thr	Gly	Leu	Pro	Gln	Arg	Ser	Gly	Ser	Asn	Ile	Glu	Gln	Tyr	Ile	
			405					410						415		
His	Asp	Leu	Asp	Ser	Asn	Ser	Phe	Glu	Leu	Asp	Leu	Gln	Phe	Ser	Glu	
		420					425					430				
Asp	Glu	Lys	Arg	Leu	Leu	Leu	Glu	Lys	Gln	Ala	Gly	Gly	Asn	Pro	Trp	
	435						440					445				
His	Gln	Phe	Val	Glu	Asn	Asn	Leu	Ile	Leu	Lys	Met	Gly	Pro	Val	Asp	
	450					455					460					
Lys	Arg	Lys	Gly	Leu	Phe	Ala	Arg	Arg	Arg	Gln	Leu	Leu	Leu	Thr	Glu	
465				470						475					480	
Gly	Pro	His	Leu	Tyr	Tyr	Val	Asp	Pro	Val	Asn	Lys	Val	Leu	Lys	Gly	
			485					490						495		
Glu	Ile	Pro	Trp	Ser	Gln	Glu	Leu	Arg	Pro	Glu	Ala	Lys	Asn	Phe	Lys	
		500						505					510			
Thr	Phe	Phe	Val	His	Thr	Pro	Asn	Arg	Thr	Tyr	Tyr	Leu	Met	Asp	Pro	
	515						520					525				
Ser	Gly	Asn	Ala	His	Lys	Trp	Cys	Arg	Lys	Ile	Gln	Glu	Val	Trp	Arg	
	530					535					540					
Gln	Arg	Tyr	Gln	Ser	His	Pro	Asp	Ala	Ala	Val	Gln					
545				550						555						

$$\begin{array}{ll} \langle 210 \rangle & 32 \\ \langle 211 \rangle & 984 \end{array}$$

<212> PRT

<213> Homo sapiens

<220>

<223> PRK2 sequence

<400> 32

Met Ala Ser Asn Pro Glu Arg Gly Glu Ile Leu Leu Thr Glu Leu Gln
1 5 10 15

Gly Asp Ser Arg Ser Leu Pro Phe Ser Glu Asn Val Ser Ala Val Gln
20 25 30

Lys Leu Asp Phe Ser Asp Thr Met Val Gln Gln Lys Leu Asp Asp Ile
35 40 45

Lys Asp Arg Ile Lys Arg Glu Ile Arg Lys Glu Leu Lys Ile Lys Glu
50 55 60

Gly Ala Glu Asn Leu Arg Lys Val Thr Thr Asp Lys Lys Ser Leu Ala
65 70 75 80

Tyr Val Asp Asn Ile Leu Lys Lys Ser Asn Lys Lys Leu Glu Glu Leu
85 90 95

His His Lys Leu Gln Glu Leu Asn Ala His Ile Val Val Ser Asp Pro
100 105 110

Glu Asp Ile Thr Asp Cys Pro Arg Thr Pro Asp Thr Pro Asn Asn Asp
115 120 125

Pro Arg Cys Ser Thr Ser Asn Asn Arg Leu Lys Ala Leu Gln Lys Gln
130 135 140

Leu Asp Ile Glu Leu Lys Val Lys Gln Gly Ala Glu Asn Met Ile Gln
145 150 155 160

Met Tyr Ser Asn Gly Ser Ser Lys Asp Arg Lys Leu His Gly Thr Ala
165 170 175

Gln Gln Leu Leu Gln Asp Ser Lys Thr Lys Ile Glu Val Ile Arg Met
180 185 190

Gln Ile Leu Gln Ala Val Gln Thr Asn Glu Leu Ala Phe Asp Asn Ala
195 200 205

Lys Pro Val Ile Ser Pro Leu Glu Leu Arg Met Glu Glu Leu Arg His
210 215 220

His	Phe	Arg	Ile	Glu	Phe	Ala	Val	Ala	Glu	Gly	Ala	Lys	Asn	Val	Met
225						230					235				240
Lys	Leu	Leu	Gly	Ser	Gly	Lys	Val	Thr	Asp	Arg	Lys	Ala	Leu	Ser	Glu
				245					250					255	
Ala	Gln	Ala	Arg	Phe	Asn	Glu	Ser	Ser	Gln	Lys	Leu	Asp	Leu	Leu	Lys
			260					265	\				270		
Tyr	Ser	Leu	Glu	Gln	Arg	Leu	Asn	Glu	Val	Pro	Lys	Asn	His	Pro	Lys
		275					280					285			
Ser	Arg	Ile	Ile	Ile	Glu	Glu	Leu	Ser	Leu	Val	Ala	Ala	Ser	Pro	Thr
	290						295				300				
Leu	Ser	Pro	Arg	Gln	Ser	Met	Ile	Ser	Thr	Gln	Asn	Gln	Tyr	Ser	Thr
305					310					315					320
Leu	Ser	Lys	Pro	Ala	Ala	Leu	Thr	Gly	Thr	Leu	Glu	Val	Arg	Leu	Met
				325					330					335	
Gly	Cys	Gln	Asp	Ile	Leu	Glu	Asn	Val	Pro	Gly	Arg	Ser	Lys	Ala	Thr
			340					345					350		
Ser	Val	Ala	Leu	Pro	Gly	Trp	Ser	Pro	Ser	Glu	Thr	Arg	Ser	Ser	Phe
		355					360					365			
Met	Ser	Arg	Thr	Ser	Lys	Ser	Lys	Ser	Gly	Ser	Ser	Arg	Asn	Leu	Leu
	370					375					380				
Lys	Thr	Asp	Asp	Leu	Ser	Asn	Asp	Val	Cys	Ala	Val	Leu	Lys	Leu	Asp
385					390					395					400
Asn	Thr	Val	Val	Gly	Gln	Thr	Ser	Trp	Lys	Pro	Ile	Ser	Asn	Gln	Ser
				405					410					415	
Trp	Asp	Gln	Lys	Phe	Thr	Leu	Glu	Leu	Asp	Arg	Ser	Arg	Glu	Leu	Glu
			420					425					430		
Ile	Ser	Val	Tyr	Trp	Arg	Asp	Trp	Arg	Ser	Leu	Cys	Ala	Val	Lys	Phe
		435					440					445			
Leu	Arg	Leu	Glu	Asp	Phe	Leu	Asp	Asn	Gln	Arg	His	Gly	Met	Cys	Leu
	450					455					460				
Tyr	Leu	Glu	Pro	Gln	Gly	Thr	Leu	Phe	Ala	Glu	Val	Thr	Phe	Phe	Asn
465					470					475					480

Pro	Val	Ile	Glu	Arg	Arg	Pro	Lys	Leu	Gln	Arg	Gln	Lys	Lys	Ile	Phe						
				485								490								495	
Ser	Lys	Gln	Gln	Gly	Lys	Thr	Phe	Leu	Arg	Ala	Pro	Gln	Met	Asn	Ile						
				500								505								510	
Asn	Ile	Ala	Thr	Trp	Gly	Arg	Leu	Val	Arg	Arg	Ala	Ile	Pro	Thr	Val						
				515								520								525	
Asn	His	Ser	Gly	Thr	Phe	Ser	Pro	Gln	Ala	Pro	Val	Pro	Thr	Thr	Val						
				530								535								540	
Pro	Val	Val	Asp	Val	Arg	Ile	Pro	Gln	Leu	Ala	Pro	Pro	Ala	Ser	Asp						
545								550								555				560	
Ser	Thr	Val	Thr	Lys	Leu	Asp	Phe	Asp	Leu	Glu	Pro	Glu	Pro	Pro	Pro						
				565								570								575	
Ala	Pro	Pro	Arg	Ala	Ser	Ser	Leu	Gly	Glu	Ile	Asp	Glu	Ser	Ser	Glu						
				580								585								590	
Leu	Arg	Val	Leu	Asp	Ile	Pro	Gly	Gln	Asp	Ser	Glu	Thr	Val	Phe	Asp						
				595								600								605	
Ile	Gln	Asn	Asp	Arg	Asn	Ser	Ile	Leu	Pro	Lys	Ser	Gln	Ser	Glu	Tyr						
				610								615								620	
Lys	Pro	Asp	Thr	Pro	Gln	Ser	Gly	Leu	Glu	Tyr	Ser	Gly	Ile	Gln	Glu						
625								630								635				640	
Leu	Glu	Asp	Arg	Arg	Ser	Gln	Gln	Arg	Phe	Gln	Phe	Asn	Leu	Gln	Asp						
				645								650								655	
Phe	Arg	Cys	Cys	Ala	Val	Leu	Gly	Arg	Gly	His	Phe	Gly	Lys	Val	Leu						
				660								665								670	
Leu	Ala	Glu	Tyr	Lys	Asn	Thr	Asn	Glu	Met	Phe	Ala	Ile	Lys	Ala	Leu						
				675								680								685	
Lys	Lys	Gly	Asp	Ile	Val	Ala	Arg	Asp	Glu	Val	Asp	Ser	Leu	Met	Cys						
690								695								700					
Glu	Lys	Arg	Ile	Phe	Glu	Thr	Val	Asn	Ser	Val	Arg	His	Pro	Phe	Leu						
705								710								715				720	
Val	Asn	Leu	Phe	Ala	Cys	Phe	Gln	Thr	Lys	Glu	His	Val	Cys	Phe	Val						
				725								730								735	

[illegible]

Met	Glu	Tyr	Ala	Ala	Gly	Gly	Asp	Leu	Met	Met	His	Ile	His	Thr	Asp		
			740						745						750		
Val	Phe	Ser	Glu	Pro	Arg	Ala	Val	Phe	Tyr	Ala	Ala	Cys	Val	Val	Leu		
			755						760						765		
Gly	Leu	Gln	Tyr	Leu	His	Glu	His	Lys	Ile	Val	Tyr	Arg	Asp	Leu	Lys		
			770						775						780		
Leu	Asp	Asn	Leu	Leu	Leu	Asp	Thr	Glu	Gly	Phe	Val	Lys	Ile	Ala	Asp		
785						790						795			800		
Phe	Gly	Leu	Cys	Lys	Glu	Gly	Met	Gly	Tyr	Gly	Asp	Arg	Thr	Ser	Thr		
			805						810						815		
Phe	Cys	Gly	Thr	Pro	Glu	Phe	Leu	Ala	Pro	Glu	Val	Leu	Thr	Glu	Thr		
			820						825						830		
Ser	Tyr	Thr	Arg	Ala	Val	Asp	Trp	Trp	Gly	Leu	Gly	Val	Leu	Ile	Tyr		
			835						840						845		
Glu	Met	Leu	Val	Gly	Glu	Ser	Pro	Phe	Pro	Gly	Asp	Asp	Glu	Glu	Glu		
850						855						860					
Val	Phe	Asp	Ser	Ile	Val	Asn	Asp	Glu	Val	Arg	Tyr	Pro	Arg	Phe	Leu		
865						870						875			880		
Ser	Thr	Glu	Ala	Ile	Ser	Ile	Met	Arg	Arg	Leu	Leu	Arg	Arg	Asn	Pro		
			885						890						895		
Glu	Arg	Arg	Leu	Gly	Ala	Ser	Glu	Lys	Asp	Ala	Glu	Asp	Val	Lys	Lys		
			900						905						910		
His	Pro	Phe	Phe	Arg	Leu	Ile	Asp	Trp	Ser	Ala	Leu	Met	Asp	Lys	Lys		
			915						920						925		
Val	Lys	Pro	Pro	Phe	Ile	Pro	Thr	Ile	Arg	Gly	Arg	Glu	Asp	Val	Ser		
930						935						940					
Asn	Phe	Asp	Asp	Glu	Phe	Thr	Ser	Glu	Ala	Pro	Ile	Leu	Thr	Pro	Pro		
945						950						955			960		
Arg	Glu	Pro	Arg	Ile	Leu	Ser	Glu	Glu	Glu	Gln	Glu	Met	Phe	Arg	Asp		
			965						970						975		
Phe	Asp	Tyr	Ile	Ala	Asp	Trp	Cys										
			980														

```
<210> 33
<211> 942
<212> PRT
<213> Homo sapiens
```

<220>
<223> PRK1 sequence

```

<400> 33
Met Ala Ser Asp Ala Val Gln Ser Glu Pro Arg Ser Trp Ser Leu Leu
  1             5             10             15
Glu Gln Leu Gly Leu Ala Gly Ala Asp Leu Ala Ala Pro Gly Val Gln
      20             25             30
Gln Gln Leu Glu Leu Glu Arg Glu Arg Leu Arg Arg Glu Ile Arg Lys
      35             40             45
Glu Leu Lys Leu Lys Glu Gly Ala Glu Asn Leu Arg Arg Ala Thr Thr
      50             55             60
Asp Leu Gly Arg Ser Leu Gly Pro Val Glu Leu Leu Leu Arg Gly Ser
      65             70             75             80
Ser Arg Arg Leu Asp Leu Leu His Gln Gln Leu Gln Glu Leu His Ala
      85             90             95
His Val Val Leu Pro Asp Pro Ala Ala Thr His Asp Gly Pro Gln Ser
      100             105             110
Pro Gly Ala Gly Gly Pro Thr Cys Ser Ala Thr Asn Leu Ser Arg Val
      115             120             125
Ala Gly Leu Glu Lys Gln Leu Ala Ile Glu Leu Lys Val Lys Gln Gly
      130             135             140
Ala Glu Asn Met Ile Gln Thr Tyr Ser Asn Gly Ser Thr Lys Asp Arg
      145             150             155             160
Lys Leu Leu Leu Thr Ala Gln Gln Met Leu Gln Asp Ser Lys Thr Lys
      165             170             175
Ile Asp Ile Ile Arg Met Gln Leu Arg Arg Ala Leu Gln Ala Asp Gln
      180             185             190
Leu Glu Asn Gln Ala Ala Pro Asp Asp Thr Gln Gly Ser Pro Asp Leu

```

195	200	205
Gly Ala Val Glu Leu Arg Ile Glu Glu Leu Arg His His Phe Arg Val		
210	215	220
Glu His Ala Val Ala Glu Gly Ala Lys Asn Val Leu Arg Leu Leu Ser		
225	230	235 240
Ala Ala Lys Ala Pro Asp Arg Lys Ala Val Ser Glu Ala Gln Glu Lys		
	245	250 255
Leu Thr Glu Ser Asn Gln Lys Leu Gly Leu Leu Arg Glu Ala Leu Glu		
	260	265 270
Arg Arg Leu Gly Glu Leu Pro Ala Asp His Pro Lys Gly Arg Leu Leu		
	275	280 285
Arg Glu Glu Leu Ala Ala Ala Ser Ser Ala Ala Phe Ser Thr Arg Leu		
	290	295 300
Ala Gly Pro Phe Pro Ala Thr His Tyr Ser Thr Leu Cys Lys Pro Ala		
305	310	315 320
Pro Leu Thr Gly Thr Leu Glu Val Arg Val Val Gly Cys Arg Asp Leu		
	325	330 335
Pro Glu Thr Ile Pro Trp Asn Pro Thr Pro Ser Met Gly Gly Pro Gly		
	340	345 350
Thr Pro Asp Ser Arg Pro Pro Phe Leu Ser Arg Pro Ala Arg Gly Leu		
	355	360 365
Tyr Ser Arg Ser Gly Ser Leu Ser Gly Arg Ser Ser Leu Lys Ala Glu		
	370	375 380
Ala Glu Asn Thr Ser Glu Val Ser Thr Val Leu Lys Leu Asp Asn Thr		
385	390	395 400
Val Val Gly Gln Thr Ser Trp Lys Pro Cys Gly Pro Asn Ala Trp Asp		
	405	410 415
Gln Ser Phe Thr Leu Glu Leu Glu Arg Ala Arg Glu Leu Glu Leu Ala		
	420	425 430
Val Phe Trp Arg Asp Gln Arg Gly Leu Cys Ala Leu Lys Phe Leu Lys		
	435	440 445
Leu Glu Asp Phe Leu Asp Asn Glu Arg His Glu Val Gln Leu Asp Met		

Leu His Ile His Ser Asp Val Phe Ser Glu Pro Arg Ala Ile Phe Tyr

U.S. DEPARTMENT OF AGRICULTURE

705					710					715					720
Ser	Ala	Cys	Val	Val	Leu	Gly	Leu	Gln	Phe	Leu	His	Glu	His	Lys	Ile
				725					730					735	
Val	Tyr	Arg	Asp	Leu	Lys	Leu	Asp	Asn	Leu	Leu	Leu	Asp	Thr	Glu	Gly
				740					745					750	
Tyr	Val	Lys	Ile	Ala	Asp	Phe	Gly	Leu	Cys	Lys	Glu	Gly	Met	Gly	Tyr
				755					760					765	
Gly	Asp	Arg	Thr	Ser	Thr	Phe	Cys	Gly	Thr	Pro	Glu	Phe	Leu	Ala	Pro
				770					775					780	
Glu	Val	Leu	Thr	Asp	Thr	Ser	Tyr	Thr	Arg	Ala	Val	Asp	Trp	Trp	Gly
785					790					795					800
Leu	Gly	Val	Leu	Leu	Tyr	Glu	Met	Leu	Val	Gly	Glu	Ser	Pro	Phe	Pro
				805					810					815	
Gly	Asp	Asp	Glu	Glu	Glu	Val	Phe	Asp	Ser	Ile	Val	Asn	Asp	Glu	Val
				820					825					830	
Arg	Tyr	Pro	Arg	Phe	Leu	Ser	Ala	Glu	Ala	Ile	Gly	Ile	Met	Arg	Arg
				835					840					845	
Leu	Leu	Arg	Arg	Asn	Pro	Glu	Arg	Arg	Leu	Gly	Ser	Ser	Glu	Arg	Asp
				850					855					860	
Ala	Glu	Asp	Val	Lys	Lys	Gln	Pro	Phe	Phe	Arg	Thr	Leu	Gly	Trp	Glu
865					870					875					880
Ala	Leu	Leu	Ala	Arg	Arg	Leu	Pro	Pro	Pro	Phe	Val	Pro	Thr	Leu	Ser
				885					890					895	
Gly	Arg	Thr	Asp	Val	Ser	Asn	Phe	Asp	Glu	Glu	Phe	Thr	Gly	Glu	Ala
				900					905					910	
Pro	Thr	Leu	Ser	Pro	Pro	Arg	Asp	Ala	Arg	Pro	Leu	Thr	Ala	Ala	Glu
				915					920					925	
Gln	Ala	Ala	Phe	Leu	Asp	Phe	Asp	Phe	Val	Ala	Gly	Gly	Cys		
				930					935					940	

```
<210> 34
<211> 592
<212> PRT
```


$\frac{1}{\sqrt{\pi}} \left(\frac{1}{\sqrt{\pi}} \right)^n \left(\frac{1}{\sqrt{\pi}} \right)^m \left(\frac{1}{\sqrt{\pi}} \right)^k \left(\frac{1}{\sqrt{\pi}} \right)^l \left(\frac{1}{\sqrt{\pi}} \right)^p \left(\frac{1}{\sqrt{\pi}} \right)^q \left(\frac{1}{\sqrt{\pi}} \right)^r \left(\frac{1}{\sqrt{\pi}} \right)^s \left(\frac{1}{\sqrt{\pi}} \right)^t \left(\frac{1}{\sqrt{\pi}} \right)^u \left(\frac{1}{\sqrt{\pi}} \right)^v \left(\frac{1}{\sqrt{\pi}} \right)^w \left(\frac{1}{\sqrt{\pi}} \right)^x \left(\frac{1}{\sqrt{\pi}} \right)^y \left(\frac{1}{\sqrt{\pi}} \right)^z$

Lys	Asp	Asp	Ser	Glu	Asp	Leu	Lys	Pro	Val	Ile	Asp	Gly	Met	Asp	Gly
225					230					235					240
Ile	Lys	Ile	Ser	Gln	Gly	Leu	Gly	Leu	Gln	Asp	Phe	Asp	Leu	Ile	Arg
				245					250					255	
Val	Ile	Gly	Arg	Gly	Thr	Tyr	Ala	Lys	Val	Leu	Leu	Val	Arg	Leu	Lys
			260					265					270		
Lys	Asn	Asp	Gln	Ile	Tyr	Ala	Met	Lys	Val	Val	Lys	Lys	Glu	Leu	Val
		275					280					285			
His	Asp	Asp	Glu	Asp	Ile	Asp	Trp	Val	Gln	Thr	Glu	Lys	His	Val	Phe
	290					295					300				
Glu	Gln	Ala	Ser	Ser	Asn	Pro	Phe	Leu	Val	Gly	Leu	His	Ser	Cys	Phe
305					310					315					320
Gln	Thr	Thr	Ser	Arg	Leu	Phe	Leu	Val	Ile	Glu	Tyr	Val	Asn	Gly	Gly
				325					330					335	
Asp	Leu	Met	Phe	His	Met	Gln	Arg	Gln	Arg	Lys	Leu	Pro	Glu	Glu	His
			340					345					350		
Ala	Arg	Phe	Tyr	Ala	Ala	Glu	Ile	Cys	Ile	Ala	Leu	Asn	Phe	Leu	His
		355					360					365			
Glu	Arg	Gly	Ile	Ile	Tyr	Arg	Asp	Leu	Lys	Leu	Asp	Asn	Val	Leu	Leu
	370					375					380				
Asp	Ala	Asp	Gly	His	Ile	Lys	Leu	Thr	Asp	Tyr	Gly	Met	Cys	Lys	Glu
385					390					395					400
Gly	Leu	Gly	Pro	Gly	Asp	Thr	Thr	Ser	Thr	Phe	Cys	Gly	Thr	Pro	Asn
				405					410					415	
Tyr	Ile	Ala	Pro	Glu	Ile	Leu	Arg	Gly	Glu	Glu	Tyr	Gly	Phe	Ser	Val
			420					425					430		
Asp	Trp	Trp	Ala	Leu	Gly	Val	Leu	Met	Phe	Glu	Met	Met	Ala	Gly	Arg
		435					440					445			
Ser	Pro	Phe	Asp	Ile	Ile	Thr	Asp	Asn	Pro	Asp	Met	Asn	Thr	Glu	Asp
	450					455					460				
Tyr	Leu	Phe	Gln	Val	Ile	Leu	Glu	Lys	Pro	Ile	Arg	Ile	Pro	Arg	Phe
465					470					475					480

[Faint, illegible markings]

Leu Ser Val Lys Ala Ser His Val Leu Lys Gly Phe Leu Asn Lys Asp
485 490 495

Pro Lys Glu Arg Leu Gly Cys Arg Pro Gln Thr Gly Phe Ser Asp Ile
500 505 510

Lys Ser His Ala Phe Phe Arg Ser Ile Asp Trp Asp Leu Leu Glu Lys
515 520 525

Lys Gln Ala Leu Pro Pro Phe Gln Pro Gln Ile Thr Asp Asp Tyr Gly
530 535 540

Leu Asp Asn Phe Asp Thr Gln Phe Thr Ser Glu Pro Val Gln Leu Thr
545 550 555 560

Pro Asp Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser Glu Phe Glu
565 570 575

Gly Phe Glu Tyr Ile Asn Pro Leu Leu Leu Ser Thr Glu Glu Ser Val
580 585 590